

This study analyzes the epidemic spread of a COVID-19-like infectious disease using the Susceptible-Infected-Recovered Introduction Mathematical modeling of infectious diseases has become a foundational tool for public health, especially Methodology Epidemic Scenario and Mechanistic Model We modeled an epidemic scenario mimicking COVID-19 spread

**Compartment Model:** SIR

**S:** Susceptible

**I:** Infected

**R:** Recovered/Removed

**Transitions:**  $S\beta I\gamma R$

Network Structure A static ER network with  $N = 1000$  nodes and average degree  $\langle k \rangle = 8$  was constructed. This reflect

Simulation Framework Simulations employed a stochastic, continuous-time implementation (FastGEMF package) to mo

with  $\gamma = 0.1$  and computed  $\beta$  accordingly.

Metrics Extracted Simulated time series were analyzed for the following metrics:

Peak Infection Rate: Maximum fraction of infected individuals

Epidemic Duration: Time from first infection to extinction

Final Epidemic Size: Total proportion recovered

Peak Time: Time to reach maximum infected

Simulation results and corresponding codebases were archived for transparency.

Results [!ht] [width=0.49]results-11.png Epidemic dynamics in the S, I, and R compartments over time for one stochast

Population Dynamics Figure depicts the temporal evolution of the S, I, and R compartments. The infection curve show

	Metric	Value
Key Metrics [!ht] Epidemic Metrics from Simulation	Peak Infection Rate	28.8%
	Peak Time (days)	19
	Epidemic Duration	62
	Final Epidemic Size	77.4%

Table summarizes the extracted epidemiological metrics. The epidemic peaks quickly and resolves within two months

Evaluation Reasoning Metrics were chosen for their epidemiological relevance and measurability from simulation output

Discussion The simulation confirms theory: random networks like ER permit rapid epidemic growth if  $R_0 > 1$  and mea

Notably, our analysis supports that topology alone, even random, significantly shapes epidemic curves—a pattern robu

Limitations Our static, ER-based model does not capture time-varying contacts, clustering, or network heterogeneity ty

Conclusion This study demonstrates that the static contact topology of an Erdős-Rényi network plays a pivotal role in

References 10

Kiss, I. Z., Miller, J. C., & Simon, P. L., *Mathematics of Epidemics on Networks: From Exact to Approximate Models*, Sprin

He, X. et al., "Temporal dynamics in viral shedding and transmissibility of COVID-19," *Nature Medicine*, vol. 26, no. 5, pp

Pastor-Satorras, R. et al., "Epidemic processes in complex networks," *Reviews of Modern Physics*, vol. 87, no. 3, pp. 925-9

Appendices Code Excerpts Key code used for simulation (full codebase available upon request):

```
import fastgemf as fg
import networkx as nx
import scipy.sparse as sparse
```

```
# Network construction
```

```
G = nx.erdos_renyi_graph(n=1000, p=8/999)
```

```
sparse.save_npz("output/network.npz", nx.to_scipy_sparse_array(G))
```

```
# Model schema and configuration (SIR-model)
```

```
SIR_schema = fg.ModelSchema("SIR").define_compartment(['S', 'I', 'R'])
```

```
... (refer to Methodology for details) ...
```

Supplementary Figures [!ht] [width=0.49]results-11.png Detailed view of epidemic compartment evolution from the stochast